



## SEQUENCE LISTING

<110> Itadani, Hiraku  
Takimura, Tetsuo  
Nakamura, Takao  
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Tanaka, Ken-ichi  
Hidaka, Yusuke  
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<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
BINDING PROTEIN-COUPLED RECEPTOR PROTEINS

<130> 06501-083001

<140> 09/891,053

<141> 2001-06-25

<150> PCT/JP99/07280

<151> 1999-12-24

<150> PCT/JP98/05967

<151> 1998-12-25

<150> JP 11/145661

<151> 1999-05-25

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 413

<212> PRT

<213> Rattus norvegicus

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Trp	Thr	Ala	Val	Leu	Ala	Ala	Leu	Met	Ala	Leu	Leu	Ile	Val	Ala	Thr
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Val	Leu	Gly	Asn	Ala	Leu	Val	Met	Leu	Ala	Phe	Val	Ala	Asp	Ser	Ser
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65				70						75				80	
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Thr	Gly	Arg	Trp	Thr	Phe	Gly	Arg	Gly	Leu	Cys	Lys	Leu	Trp	Leu	Val
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Ser	Tyr	Asp	Arg	Phe	Leu	Ser	Val	Thr	Arg	Ala	Val	Ser	Tyr	Arg	Ala

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Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr				160
	165		170	175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe				
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Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe				
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Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn				
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Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly				
225		230		235
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro				240
	245		250	255
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu				
	260		265	270
His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu				
	275		280	285
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg				
	290		295	300
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg				
305		310		315
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly				
	325		330	335
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys				
	340		345	350
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu				
	355		360	365
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His				
	370		375	380
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu				
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Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys				400
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&lt;211&gt; 1239

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&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1239)

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gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc	96
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala	
20 25 30	
tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca	144
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr	
35 40 45	

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tgg agc Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser 50 55 60	192
ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp 65 70 75 80	240
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acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val 100 105 110	336
gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile 115 120 125	384
agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala 130 135 140	432
cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp 145 150 155 160	480
gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr 165 170 175	528
ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe 180 185 190	576
ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe 195 200 205	624
acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn 210 215 220	672
atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly 225 230 235 240	720
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro 245 250 255	768
agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu 260 265 270	816

cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc 864  
 His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu  
           275                          280                          285

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc 912  
 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg  
           290                          295                          300

atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tgg cgg 960  
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           305                          310                          315                          320

gac aag aag gtg gcc aag tgg ctg gcc atc atc gtg agc atc ttt ggg 1008  
 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly  
                                   325                          330                          335

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc 1056  
 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys  
                                   340                          345                          350

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1104  
 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu  
                                   355                          360                          365

ctg tgg gcc aac tgg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1152  
 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His  
           370                          375                          380

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1200  
 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu  
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aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag 1239  
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<213> Artificial Sequence

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<223> artificially synthesized primer sequence

<221> misc\_feature

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<223> n = A,T,C or G

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21

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<223> artificially synthesized primer sequence

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4221> misc_feature
4222> (1) ... (20)
4223> n = A, T, C or G

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<210> 5
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<212> DNA
<213> Rattus norvegicus
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<222> (351)...(1589)
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<223> n = A,T,C or G
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cgccccactc	cgctcagatt	ccgacaccag	ccccctctgg	atgcacctcc	tggactctag		180
cccgggctct	tgtcccgacc	ccgcggacca	tgtccggggc	gccccccgga	aaaccgggct		240
gggcgaagag	ccggcaaaga	ttaggctcac	gagcgggggc	cccacccggc	caccagctcc		300
tccgcccgtg	ccctgcccg	tgtccccgag	ccgtgtgagc	ctgctggggc	atg gag		356
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					1		

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Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly  
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gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc 452  
Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr  
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gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg 500  
Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu  
35 40 45 50

ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc 548  
Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg  
55 60 65

acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc 596  
Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu  
70 75 80

gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc 644  
Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly  
85 90 95

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ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu 150 155 160	836
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agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu 230 235 240	1076
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Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly Leu Cys  
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 Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Lys His Gly  
 340 345 350  
 cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg att ctg tgg 1450  
 Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp  
 355 360 365 370  
 gcc aac tgg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac tac agc 1508  
 Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser  
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 Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val  
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 405 410  
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<212> DNA

<213> Artificial Sequence

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<400> 7

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32

<210> 8

<211> 25

<212> DNA

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<223> artificially synthesized primer sequence

<400> 8

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25

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<212> DNA

<213> Artificial Sequence

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21

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

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20

<210> 11

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (280)...(557)

<221> misc\_feature

<222> (1)...(1350)

<223> n = A,T,C or G

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60

120



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<210> 12

<211> 448

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (259) ... (425)

<400> 12

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<212> DNA

<213> Homo sapiens

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<221> exon

<222> (293) ... (1209)

<400> 13

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cgcttgccat	ggccactgct	tccttgacta	ctggtaagaa	acctccttct	ggctcctgtg	1080
ggccaaactcg	gctgtcaacc	ctgtcctcta	cctctgtgtc	caaccacagct	tcgcgcgggc	1140
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ctgctggaag	tgagtggccc	accagagcct	cctcagcga	cgctctcttc	agcccaggtc	1260
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cgtgtctgtg	gccctctctt	aatgccacgg	cagccaccc	gcctatggagg	cgccttctctg	1380
ggttgggcag	agggcccttc	actggttgga	ctggaggctg	ggtggccggc	cctgcccccc	1440
acattctggc	tccaccggga	gggacagtct	ggaggtccca	gacatgctgc	ccacccctctg	1500
ctggtgcccc	cccttcgcag	ttactgggtg	gtgttcttcc	caaagcaagc	acctgggtgt	1560
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gggtgttttc	agaaagatga	agaagaaaac	atgtctgtga	acttgatgtt	cctgggatgt	1860
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&lt;210&gt; 14

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; artificially synthesized primer sequence

&lt;400&gt; 14

tgaacgcttc gggggcgctg

20

&lt;210&gt; 15

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; artificially synthesized primer sequence

&lt;400&gt; 15

gagatggcga ggttgagcag g

21

&lt;210&gt; 16

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; artificially synthesized primer sequence

<400> 15  
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<210> 17  
<211> 20  
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<220>  
<223> artificially synthesized primer sequence

<400> 17  
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<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 18  
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<210> 19  
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<212> DNA  
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<220>  
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<210> 20  
<211> 453  
<212> PRT  
<213> Homo sapiens

<400> 20  
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20 25 30  
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr  
35 40 45  
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser  
50 55 60  
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp  
65 70 75 80  
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu  
85 90 95  
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val  
100 105 110  
Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

115	120	125
Ser Tyr Asp Arg Phe Leu	Ser Val Thr Arg Ala Val	Ser Tyr Arg Ala
130	135	140
Gln Gln Gly Asp Thr Arg	Arg Ala Val Arg Lys Met	Leu Leu Val Trp
145	150	155
Val Leu Ala Phe Leu Leu	Tyr Gly Pro Ala Ile	Leu Ser Trp Glu Tyr
165	170	175
Leu Ser Gly Gly Ser Ser	Ile Pro Glu Gly His Cys	Tyr Ala Glu Phe
180	185	190
Phe Tyr Asn Trp Tyr Phe	Leu Ile Thr Ala Ser Thr	Leu Glu Phe Phe
195	200	205
Thr Pro Phe Leu Ser Val	Thr Phe Phe Asn Leu Ser	Ile Tyr Leu Asn
210	215	220
Ile Gln Arg Arg Thr Arg	Leu Arg Leu Asp Gly Ala	Arg Glu Ala Ala
225	230	235
Gly Pro Glu Pro Pro Pro	Glu Ala Gln Pro Ser Pro	Pro Pro Pro Pro
245	250	255
Gly Cys Trp Gly Cys Trp	Gln Lys Gly His Gly Glu	Ala Met Pro Leu
260	265	270
His Arg Tyr Gly Val Gly	Glu Ala Ala Val Gly Ala	Glu Ala Gly Glu
275	280	285
Ala Thr Leu Gly Gly Gly	Gly Gly Gly Gly Ser Val	Ala Ser Pro Thr
290	295	300
Ser Ser Ser Gly Ser Ser	Ser Arg Gly Thr Glu Arg	Pro Arg Ser Leu
305	310	315
Lys Arg Gly Ser Lys Pro	Ser Ala Ser Ser Leu Glu	Lys Arg
325	330	335
Met Lys Met Val Ser Gln	Ser Phe Thr Gln Arg Phe	Arg Leu Ser Arg
340	345	350
Asp Arg Lys Val Ala Lys	Ser Leu Ala Val Ile Val	Ser Ile Phe Gly
355	360	365
Leu Cys Trp Ala Pro Tyr	Thr Leu Leu Met Ile Ile	Arg Ala Ala Cys
370	375	380
His Gly His Cys Val Pro	Asp Tyr Trp Tyr Glu Thr	Ser Phe Trp Leu
385	390	395
Leu Trp Ala Asn Ser Ala	Val Asn Pro Val Leu Tyr	Pro Leu Cys His
405	410	415
His Ser Phe Arg Arg Ala	Phe Thr Lys Leu Leu Cys	Pro Gln Lys Leu
420	425	430
Lys Ile Gln Pro His Ser	Ser Leu Glu His Cys Trp	Lys Lys Met Lys
435	440	445
Lys Lys Thr Cys Leu		
450		

&lt;210&gt; 21

&lt;211&gt; 2050

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (271)...(1629)

&lt;400&gt; 21

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aggctgcgga ggcagagctg catgctgggt gcgggaagag gtgggctcgc tcgcggagtc	180

gctgagtcgcg	tgccctttta	gttagttctg	cagtctagta	tggtcccat	ttgcccttcc	240
actcccgag	cgcgctgagc	ctgcgggggc	atg gag cgc gcg ccg ccc gac ggg			294
			Met Glu Arg Ala Pro Pro Asp Gly			
			1 5			
ccg ctg aac gct teg ggg gcg ctg gcg ggc gag gcg gcg gcg gcg ggc						342
Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly						
10 15 20						
ggg gcg cgc ggc ttc teg gca gcc tgg acc gcg gtg ctg gcc gcg ctc						390
Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu						
25 30 35 40						
atg gcg ctg ctc atc gtg gcc acg gtg ctg ggc aac gcg ctg gtc atg						438
Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met						
45 50 55						
ctc gcc ttc gtg gcc gac teg agc ctc cgc acc cag aac aac ttc ttc						486
Leu Ala Phe Val Ala Asp Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe						
60 65 70						
ctg ctc aac ctc gcc atc tcc gac ttc ctc gtc ggc gcc ttc tgc atc						534
Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu Val Gly Ala Phe Cys Ile						
75 80 85						
cca ctg tat gta ccc tac gtg ctg aca ggc cgc tgg acc ttc ggc cgg						582
Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly Arg Trp Thr Phe Gly Arg						
90 95 100						
ggc ctc tgc aag ctg tgg ctg gta gtg gac tac ctg ctg tgc acc tcc						630
Gly Leu Cys Lys Leu Trp Leu Val Val Asp Tyr Leu Leu Cys Thr Ser						
105 110 115 120						
tct gcc ttc aac atc gtg ctc atc agc tac gac cgc ttc ctg teg gtc						678
Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val						
125 130 135						
acc cga gcg gtc tca tac cgg gcc cag cag ggt gac acg cgg cgg gca						726
Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala						
140 145 150						
gtg cgg aag atg ctg ctg gtg tgg gtg ctg gcc ttc ctg ctg tac gga						774
Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly						
155 160 165						
cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc						822
Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro						
170 175 180						
gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc						870
Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile						
185 190 195 200						
acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc						918
Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe						
205 210 215						

ttt aac ctc agc atc tac ctg aac atc bag agg cgc acc cgc ctc cgg Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg 220 225 230	956
ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Pro Glu Ala 235 240 245	1014
cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag Gln Pro Ser Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys 250 255 260	1062
ggg cac ggg gag gcc atg ccg ctg cac agg tat ggg gtg ggt gag gcg Gly His Gly Glu Ala Met Pro Leu His Arg Tyr Gly Val Gly Glu Ala 265 270 275 280	1110
gcc gta ggc gct gag gcc ggg gag gcg acc ctc ggg ggt ggc ggt ggg Ala Val Gly Ala Glu Ala Gly Glu Ala Thr Leu Gly Gly Gly Gly Gly 285 290 295	1158
ggc ggc tcc gtg gct tca ccc acc tcc agc tcc ggc agc tcc tcg agg Gly Gly Ser Val Ala Ser Pro Thr Ser Ser Ser Gly Ser Ser Ser Arg 300 305 310	1206
ggc act gag agg ccg cgc tca ctc aag agg ggc tcc aag ccg tcg gcg Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg Gly Ser Lys Pro Ser Ala 315 320 325	1254
tcc tcg gcc tcg ctg gag aag cgc atg aag atg gtg tcc cag agc ttc Ser Ser Ala Ser Leu Glu Lys Arg Met Lys Met Val Ser Gln Ser Phe 330 335 340	1302
acc cag cgc ttt cgg ctg tct cgg gac agg aaa gtg gcc aag tcg ctg Thr Gln Arg Phe Arg Leu Ser Arg Asp Arg Lys Val Ala Lys Ser Leu 345 350 355 360	1350
gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu 365 370 375	1398
ctg atg atc atc cgg gcc gcc tgc cat ggc cac tgc gtc cct gac tac Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr 380 385 390	1446
tgg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tcg gct gtc aac Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn 395 400 405	1494
cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr 410 415 420	1542
aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu 425 430 435 440	1590
gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat	1639

Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu  
 445 450

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gttcctggga tgtttaatca agagagacaa aattgctgag gagctcaggg ctggattggc 1699
aggtgtgggc tcccacgccc tctccctcc gctaaggett ccggtgagc tgtgccagct 1759
gcttctgccc accccgcctc tgggctcaca ccagccctgg tggccaagcc tgccccggcc 1819
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cgagggtccc aaggcgtgca ggggcgggcc agaggaggtg ccggggcagg ggccgcttcg 1939
ccatgtgctg tgcacccgtg ccacgcgctc tgcattgctc tctgctgtg ccgctgcgc 1999
tgcctgcaa accgtgaggt cacaataaag tgtatttttt tattggtgct g 2050
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<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc\_feature

<222> (1)...(20)

<223> n = A,T,C or G

<400> 22

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20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc\_feature

<222> (1)...(20)

<223> n = A,T,C or G

<400> 23

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20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 24

tgctctggga caccatcttc

20

<210> 25

<211> 445

<212> PRT

<213> Rattus norvegicus

&lt;400&gt; 25

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Ala	Gly	Glu	Ala	Ala	Ala	Ala	Gly	Gly	Ala	Arg	Gly	Phe	Ser	Ala	Ala
			20					25					30		
Trp	Thr	Ala	Val	Leu	Ala	Ala	Leu	Met	Ala	Leu	Leu	Ile	Val	Ala	Thr
		35					40					45			
Val	Leu	Gly	Asn	Ala	Leu	Val	Met	Leu	Ala	Phe	Val	Ala	Asp	Ser	Ser
	50					55					60				
Leu	Arg	Thr	Gln	Asn	Asn	Phe	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp
65					70					75					80
Phe	Leu	Val	Gly	Ala	Phe	Cys	Ile	Pro	Leu	Tyr	Val	Pro	Tyr	Val	Leu
				85					90					95	
Thr	Gly	Arg	Trp	Thr	Phe	Gly	Arg	Gly	Leu	Cys	Lys	Leu	Trp	Leu	Val
			100					105					110		
Val	Asp	Tyr	Leu	Leu	Cys	Ala	Ser	Ser	Val	Phe	Asn	Ile	Val	Leu	Ile
	115						120					125			
Ser	Tyr	Asp	Arg	Phe	Leu	Ser	Val	Thr	Arg	Ala	Val	Ser	Tyr	Arg	Ala
	130					135					140				
Gln	Gln	Gly	Asp	Thr	Arg	Arg	Ala	Val	Arg	Lys	Met	Ala	Leu	Val	Trp
145					150					155					160
Val	Leu	Ala	Phe	Leu	Leu	Tyr	Gly	Pro	Ala	Ile	Leu	Ser	Trp	Glu	Tyr
			165					170					175		
Leu	Ser	Gly	Gly	Ser	Ser	Ile	Pro	Glu	Gly	His	Cys	Tyr	Ala	Glu	Phe
		180						185					190		
Phe	Tyr	Asn	Trp	Tyr	Phe	Leu	Ile	Thr	Ala	Ser	Thr	Leu	Glu	Phe	Phe
	195					200						205			
Thr	Pro	Phe	Leu	Ser	Val	Thr	Phe	Phe	Asn	Leu	Ser	Ile	Tyr	Leu	Asn
	210					215					220				
Ile	Gln	Arg	Arg	Thr	Arg	Leu	Arg	Leu	Asp	Gly	Gly	Arg	Glu	Ala	Gly
225					230					235					240
Pro	Glu	Pro	Pro	Pro	Asp	Ala	Gln	Pro	Ser	Pro	Pro	Pro	Ala	Pro	Pro
				245					250					255	
Ser	Cys	Trp	Gly	Cys	Trp	Pro	Lys	Gly	His	Gly	Glu	Ala	Met	Pro	Leu
		260						265					270		
His	Arg	Tyr	Gly	Val	Gly	Glu	Ala	Gly	Pro	Gly	Val	Glu	Ala	Gly	Glu
	275						280					285			
Ala	Ala	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ala	Ala	Ala	Ser	Pro	Thr
	290					295					300				
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Arg	Gly	Thr	Glu	Arg	Pro	Arg	Ser	Leu
305					310				315						320
Lys	Arg	Gly	Ser	Lys	Pro	Ser	Ala	Ser	Ser	Ala	Ser	Leu	Glu	Lys	Arg
			325					330					335		
Met	Lys	Met	Val	Ser	Gln	Ser	Ile	Thr	Gln	Arg	Phe	Arg	Leu	Ser	Arg
		340						345					350		
Asp	Lys	Lys	Val	Ala	Lys	Ser	Leu	Ala	Ile	Ile	Val	Ser	Ile	Phe	Gly
	355						360					365			
Leu	Cys	Trp	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Ile	Ile	Arg	Ala	Ala	Cys
	370					375					380				
His	Gly	Arg	Cys	Ile	Pro	Asp	Tyr	Trp	Tyr	Glu	Thr	Ser	Phe	Trp	Leu
385					390					395					400
Leu	Trp	Ala	Asn	Ser	Ala	Val	Asn	Pro	Val	Leu	Tyr	Pro	Leu	Cys	His
			405						410					415	
Tyr	Ser	Phe	Arg	Arg	Ala	Phe	Thr	Lys	Leu	Leu	Cys	Pro	Gln	Lys	Leu
		420						425					430		
Lys	Val	Gln	Pro	His	Gly	Ser	Leu	Glu	Gln	Cys	Trp	Lys			
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 <212> DNA  
 <213> Rattus norvegicus

<220>  
 <221> CDS  
 <222> (302)...(1636)

<400> 26  
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 ctggactcta gcccggtc ttgtccgac ccgcggacc atgtccggg cgcgcgcgg 180  
 aaaaccgggc tgggcgaaga gccggcaaag attaggetca cgagcggggg ccccaaccgg 240  
 ccaccagct ctccgcgcgt gccctgcccg gtgtcccca gccgtgtgag cctgctgggc 300  
 c atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg 349  
 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu  
 1 5 10 15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 397  
 Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala  
 20 25 30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 445  
 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr  
 35 40 45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc 493  
 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser  
 50 55 60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac 541  
 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp  
 65 70 75 80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg 589  
 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu  
 85 90 95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg 637  
 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val  
 100 105 110

gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc 685  
 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile  
 115 120 125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc 733  
 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala  
 130 135 140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg 781  
 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp  
 145 150 155 160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac 829

Val	Leu	Ala	Phe	Leu	Leu	Tyr	Gly	Pro	Ala	Ile	Leu	Ser	Trp	Glu	Tyr		
				165					170					175			
ctg	tct	ggg	ggc	agt	tcc	atc	ccc	gag	ggc	cac	tgc	tat	gct	gag	ttc	877	
Leu	Ser	Gly	Gly	Ser	Ser	Ile	Pro	Glu	Gly	His	Cys	Tyr	Ala	Glu	Phe		
			180					185					190				
ttc	tac	aac	tgg	tac	ttt	ctc	atc	acg	gcc	tcc	acc	ctc	gag	ttc	ttc	925	
Phe	Tyr	Asn	Trp	Tyr	Phe	Leu	Ile	Thr	Ala	Ser	Thr	Leu	Glu	Phe	Phe		
		195					200				205						
acg	ccc	ttc	ctc	agc	gtt	acc	ttc	ttc	aac	ctc	agc	atc	tac	ctg	aac	973	
Thr	Pro	Phe	Leu	Ser	Val	Thr	Phe	Phe	Asn	Leu	Ser	Ile	Tyr	Leu	Asn		
	210					215					220						
atc	cag	agg	cgc	acc	cgc	ctt	ggg	ctt	gat	ggg	ggc	cgt	gag	gct	ggc	1021	
Ile	Gln	Arg	Arg	Thr	Arg	Leu	Arg	Leu	Asp	Gly	Gly	Arg	Glu	Ala	Gly		
225					230				235					240			
cca	gaa	ccc	cca	cca	gat	gcc	cag	ccc	tcg	cca	cct	cca	gct	ccc	ccc	1069	
Pro	Glu	Pro	Pro	Pro	Asp	Ala	Gln	Pro	Ser	Pro	Pro	Pro	Ala	Pro	Pro		
				245				250					255				
agc	tgc	tgg	ggc	tgc	tgg	cca	aaa	ggg	cat	ggc	gag	gcc	atg	ccg	ttg	1117	
Ser	Cys	Trp	Gly	Cys	Trp	Pro	Lys	Gly	His	Gly	Glu	Ala	Met	Pro	Leu		
		260					265					270					
cac	agg	tat	ggg	gtg	ggg	gag	gca	ggc	cct	ggg	gtt	gag	gct	ggg	gag	1165	
His	Arg	Tyr	Gly	Val	Gly	Glu	Ala	Gly	Pro	Gly	Val	Glu	Ala	Gly	Glu		
		275				280					285						
gct	gcc	ctc	ggg	ggg	ggc	agt	ggg	gga	ggg	gct	gct	gcc	tcg	ccc	acc	1213	
Ala	Ala	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ala	Ala	Ala	Ser	Pro	Thr		
	290					295				300							
tcc	agc	tct	ggc	agc	tcc	tca	agg	ggc	act	gag	agg	cca	cgc	tca	ctc	1261	
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Arg	Gly	Thr	Glu	Arg	Pro	Arg	Ser	Leu		
305					310				315					320			
aaa	agg	ggc	tcc	aag	cca	tca	gca	tct	tca	gca	tcc	ctg	gag	aag	cgc	1309	
Lys	Arg	Gly	Ser	Lys	Pro	Ser	Ala	Ser	Ser	Ala	Ser	Leu	Glu	Lys	Arg		
			325					330				335					
atg	aag	atg	gtg	tcc	cag	agc	atc	acc	cag	cgc	ttc	cgg	ctg	tcg	cgg	1357	
Met	Lys	Met	Val	Ser	Gln	Ser	Ile	Thr	Gln	Arg	Phe	Arg	Leu	Ser	Arg		
			340				345					350					
gac	aag	aag	gtg	gcc	aag	tcg	ctg	gcc	atc	atc	gtg	agc	atc	ttt	ggg	1405	
Asp	Lys	Lys	Val	Ala	Lys	Ser	Leu	Ala	Ile	Ile	Val	Ser	Ile	Phe	Gly		
		355				360					365						
ctc	tgc	tgg	gcg	ccg	tac	acg	ctc	cta	atg	atc	atc	cga	gct	gct	tgc	1453	
Leu	Cys	Trp	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Ile	Ile	Arg	Ala	Ala	Cys		
	370					375					380						
cat	ggc	cgc	tgc	atc	ccc	gat	tac	tgg	tac	gag	acg	tcc	ttc	tgg	ctt	1501	
His	Gly	Arg	Cys	Ile	Pro	Asp	Tyr	Trp	Tyr	Glu	Thr	Ser	Phe	Trp	Leu		

335	390	395	400	
ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac				1549
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His				
	405	410	415	
tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc				1597
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu				
	420	425	430	
aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag tgagcagctg				1646
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys				
	435	440	445	
ccccaccctt ctgaggccag gcccttgtae ttgtttgagt gggcagccgg agcgtgggag				1706
gggccctggt ccatgctccg ctccaaatgc catgggggag tottagatca tcaaccccgc				1766
agtggggtag catggcaggt gggccaagag cctagttgg tggagctaga gtgtgctggt				1826
tagctctgcc gcacattctc cttcaccaca cagaagagac aatccaggag tcccaggcat				1886
gccttcacct acacacacac acacacacac acacacacac acaccacagt gcagtgccag				1946
tgatgtc				1953